

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Schlessinger, Joseph  
Sap, Jan M.

(ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE  
PHOSPHATASE-ALPHA

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: PENNIE & EDMONDS  
(B) STREET: 1155 AVENUE OF THE AMERICAS  
(C) CITY: NEW YORK  
(D) STATE: NEW YORK  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/015,985  
(B) FILING DATE: 10-FEB-1993  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Coruzzi, Laura A.  
(B) REGISTRATION NUMBER: 30,742  
(C) REFERENCE/DOCKET NUMBER: 7683-020

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 790-9090  
(B) TELEFAX: (212) 869-9741/8864  
(C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 802 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Ser	Trp	Phe	Ile	Leu	Val	Leu	Leu	Gly	Ser	Gly	Leu	Ile	Cys
1				5					10					15	
Val	Ser	Ala	Asn	Asn	Ala	Thr	Thr	Val	Ala	Pro	Ser	Val	Gly	Ile	Thr
		20					25						30		
Arg	Leu	Ile	Asn	Ser	Ser	Thr	Ala	Glu	Pro	Val	Lys	Glu	Glu	Ala	Lys
		35				40						45			
Thr	Ser	Asn	Pro	Thr	Ser	Ser	Leu	Thr	Ser	Leu	Ser	Val	Ala	Pro	Thr
	50					55					60				

Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn  
 65 70 75 80  
 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser  
 85 90 95  
 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln  
 100 105 110  
 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala  
 115 120 125  
 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys  
 130 135 140  
 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser  
 145 150 155 160  
 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg  
 165 170 175  
 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu  
 180 185 190  
 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu  
 195 200 205  
 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp  
 210 215 220  
 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu  
 225 230 235 240  
 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr  
 245 250 255  
 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val  
 260 265 270  
 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu  
 275 280 285  
 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr  
 290 295 300  
 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr  
 305 310 315 320  
 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile  
 325 330 335  
 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln  
 340 345 350  
 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser  
 355 360 365  
 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys  
 370 375 380  
 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile  
 385 390 395 400  
 Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr  
 405 410 415  
 Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro

420					425					430				
Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg	435				440					445				
Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr	450				455					460				
Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln	465				470				475				480	
Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln		485					490					495		
Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr		500					505					510		
Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr		515				520					525			
Ser Asn Asn Gly Leu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys	530			535					540					
Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys	545			550				555					560	
Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile		565					570					575		
Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val Asn Ala Ser		580				585					590			
Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly		595			600					605				
Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp	610			615					620					
Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu Arg Gly Gln	625			630				635					640	
Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly		645					650					655		
Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu Ser Tyr Thr		660				665					670			
Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln		675			680				685					
Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser	690			695				700						
Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln	705			710			715						720	
Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala		725				730					735			
Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val		740			745						750			
Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg		755			760				765					
Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys	770			775				780						

Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn  
785 790 795 800

Phe Lys

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2409 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGATTCTT	GGTTCATTCT	TGTTCTGCTC	GGCAGTGGTC	TGATATGTGT	CAGTGCCAAC	60
AATGCTACCA	CAGTTGCACC	TTCTGTAGGA	ATTACAAGAT	TAATTAAGTC	ATCAACGGCA	120
GAACCAAGTTA	AAGAAGAGGC	CAAACTTCA	AATCCAAGTT	CTTCACTAAC	TTCTCTTTCT	180
GTGGCACCAA	CATTAGCCC	AAATATAACT	CTGGGACCCA	CCTATTTAAC	CACTGTCAAT	240
TCTTCAGACT	CTGACAATGG	GACCACAAGA	ACAGCAAGCA	CCAATTCTAT	AGGCATTACA	300
ATTTACCAA	ATGGAACGTG	GCTTCCAGAT	AACCAAGTTCA	CGGATGCCAG	AACAGAACCC	360
TGGGAGGGGA	ATTCCAGCAC	CGCAGCAACC	ACTCCAGAAA	CTTTCCCTCC	TTCAGGTAAT	420
TCTGACTCGA	AGGACAGAAG	AGATGAGACA	CCAATTATTG	CGGTGATGGT	GGCCCTGTCC	480
TCTCTGCTAG	TGATCGTGTT	TATTATCATA	GTTTTGTACA	TGTTAAGGTT	TAAGAAATAC	540
AAGCAAGCTG	GGAGCCATTC	CAATTCTTTC	CGCTTATCCA	ACGGCCGCAC	TGAGGATGTG	600
GAGCCCCAGA	GTGTGCCACT	TCTGGCCAGA	TCCCCAAGCA	CCAACAGGAA	ATACCCACCC	660
CTGCCCCGTG	ACAAGCTGGA	AGAGGAAATT	AACCGGAGAA	TGGCAGACGA	CAATAAGCTC	720
TTAGGGGAGG	AATTCAACGC	TCTCCCTGCA	TGTCCTATCC	AGGCCACCTG	TGAGGCTGCT	780
TCCAAGGAGG	AAAACAAGGA	AAAAAATCGA	TATGTAAACA	TCTTGCCTTA	TGACCACTCT	840
AGAGTCCACC	TGACACCGGT	TGAAGGGGTT	CCAGATTCTG	ATTACATCAA	TGCTTCATTC	900
ATCAACGGTT	ACCAAGAAAA	GAACAAATTC	ATTGCTGCAC	AAGGACCAAA	AGAAGAAACG	960
GTGAATGATT	TCTGGCGGAT	GATCTGGGAA	CAAAACACAG	CCACCATCGT	CATGGTTACC	1020
AACCTGAAGG	AGAGAAAGGA	GTGCAAGTGC	GCCCACTACT	GGCCAGACCA	AGGCTGCTGG	1080
ACCTATGGGA	ATATTCGGGT	GTCTGTAGAG	GATGTGACTG	TCCTGGTGGA	CTACACAGTA	1140
CGGAAGTTCT	GCATCCAGCA	GGTGGGCGAC	ATGACCAACA	GAAAGCCACA	GCGCCTCATC	1200
ACTCAGTTCC	ACTTTACCAG	CTGGCCAGAC	TTTGGGGTGC	CTTTTACCCC	GATCGGCATG	1260
CTCAAGTTCC	TCAAGAAGGT	GAAGGCCTGT	AACCCCTCAGT	ATGCAGGGGC	CATCGTGGTC	1320
CACTGCAGTG	CAGGTGTAGG	GCGTACAGGT	ACCTTTGTCTG	TCATTGATGC	CATGCTGGAC	1380
ATGATGCATA	CAGAACGGAA	GGTGGACGTG	TATGGCTTTG	TGAGCCGGAT	CCGGGCACAG	1440
CGCTGCCAGA	TGGTGCAAAC	CGATATGCAG	TATGTCTTCA	TATACCAAGC	CCTTCTGGAG	1500

CATTATCTCT ATGGAGATAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA 1560  
 ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA 1620  
 ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCCAGC CAACATGAAG 1680  
 AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCAACA GAGTGATCAT TCCAGTTAAG 1740  
 CGGGGCGAAG AGAATACAGA CTATGTGAAC GCATCCTTTA TTGATGGCTA CCGGCAGAAG 1800  
 GACTCCTATA TCGCCAGOCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG 1860  
 ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG 1920  
 GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGACTGGTGT CCTATGGAGA TATTACAGTG 1980  
 GAACTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTCAACCAAC 2040  
 ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG 2100  
 GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG 2160  
 CAGCAGTCAG GGAACCACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG 2220  
 ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGGAT TTTGGATGTC 2280  
 TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG 2340  
 TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC 2400  
 TTCAAGTAA 2409

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His  
 1 5 10 15  
 Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr  
 20 25 30  
 Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys  
 35 40 45  
 Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr  
 50 55 60  
 Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn  
 65 70 75 80  
 Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser  
 85 90 95  
 Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln  
 100 105 110  
 Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala  
 115 120 125

Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile  
130 135 140

Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile  
145 150 155 160

Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser  
165 170 175

His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu  
180 185 190

Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys  
195 200 205

Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg  
210 215 220

Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro  
225 230 235 240

Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn  
245 250 255

Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg  
260 265 270

Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn  
275 280 285

Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala  
290 295 300

Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp  
305 310 315 320

Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu Arg  
325 330 335

Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Cys Trp Thr  
340 345 350

Tyr Gly Asn Val Arg Val Ser Val Glu Asp Val Thr Val Leu Val Asp  
355 360 365

Tyr Thr Val Arg Lys Phe Ser Ile Gln Gln Val Gly Asp Val Thr Asn  
370 375 380

Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp Pro  
385 390 395 400

Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys  
405 410 415

Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val His  
420 425 430

Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp Ala  
435 440 445

Met Leu Asp Met Met His Ser Glu Arg Lys Val Asp Val Tyr Gly Phe  
450 455 460

Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp Met  
465 470 475 480

Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu His Tyr Leu Tyr Gly

485										490										495																																			
Asp	Thr	Glu	Leu	Glu	Val	Thr	Ser	Leu	Glu	Thr	His	Leu	Gln	Lys	Ile																																								
			500						505				510																																										
Tyr	Asn	Lys	Ile	Pro	Gly	Thr	Ser	Asn	Asn	Gly	Leu	Glu	Glu	Glu	Phe																																								
		515					520					525																																											
Lys	Lys	Leu	Thr	Ser	Ile	Lys	Ile	Gln	Asn	Asp	Lys	Met	Arg	Thr	Gly																																								
		530				535					540																																												
Asn	Leu	Pro	Ala	Asn	Met	Lys	Lys	Asn	Arg	Val	Leu	Gln	Ile	Ile	Pro																																								
		545			550				555						560																																								
Tyr	Glu	Phe	Asn	Arg	Val	Ile	Ile	Pro	Val	Lys	Arg	Gly	Glu	Glu	Asn																																								
			565						570						575																																								
Thr	Asp	Tyr	Val	Asn	Ala	Ser	Phe	Ile	Asp	Gly	Tyr	Arg	Gln	Lys	Asp																																								
			580					585						590																																									
Ser	Tyr	Ile	Ala	Ser	Gln	Gly	Pro	Leu	Leu	His	Thr	Ile	Glu	Asp	Phe																																								
		595					600							605																																									
Trp	Arg	Met	Ile	Trp	Glu	Trp	Lys	Ser	Cys	Ser	Ile	Val	Met	Leu	Thr																																								
		610				615					620																																												
Glu	Leu	Glu	Glu	Arg	Gly	Gln	Glu	Lys	Cys	Ala	Gln	Tyr	Trp	Pro	Ser																																								
		625			630				635					640																																									
Asp	Gly	Leu	Val	Ser	Tyr	Gly	Asp	Ile	Thr	Val	Glu	Leu	Lys	Lys	Glu																																								
			645						650					655																																									
Glu	Glu	Cys	Glu	Ser	Tyr	Thr	Val	Arg	Asp	Leu	Leu	Val	Thr	Asn	Thr																																								
		660						665					670																																										
Arg	Glu	Asn	Lys	Ser	Arg	Gln	Ile	Arg	Gln	Phe	His	Phe	His	Gly	Trp																																								
		675				680						685																																											
Pro	Glu	Val	Gly	Ile	Pro	Ser	Asp	Gly	Lys	Gly	Met	Ile	Asn	Ile	Ile																																								
		690				695					700																																												
Ala	Ala	Val	Gln	Lys	Gln	Gln	Gln	Ser	Gly	Asn	His	Pro	Ile	Thr																																									
		705			710				715				720																																										
Val	His	Cys	Ser	Ala	Gly	Ala	Gly	Arg	Thr	Gly	Thr	Phe	Cys	Ala	Leu																																								
			725					730					735																																										
Ser	Thr	Val	Leu	Glu	Arg	Val	Lys	Ala	Glu	Gly	Ile	Leu	Asp	Val	Phe																																								
			740				745						750																																										
Gln	Thr	Val	Lys	Ser	Leu	Arg	Leu	Gln	Arg	Pro	His	Met	Val	Gln	Thr																																								
			755				760					765																																											
Leu	Glu	Gln	Tyr	Glu	Phe	Cys	Tyr	Lys	Val	Val	Gln	Glu	Tyr	Ile	Asp																																								
		770				775					780																																												
Ala	Phe	Ser	Asp	Tyr	Ala	Asn	Phe	Lys																																															
		785				790																																																	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2872 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown



(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGC GAGTGAGGCG CTGACAGGGA CTCGCGGGGG CATCTTGAC AGACCCCTGG	60
ACCACGCCGC CATCGCAGCC TCCAGCCCAG TCCTCTCTCT GCCGCTTCTC CTCGCCATGG	120
AGGCCGCCGA CCGCCGTCCG CGGGCTTCGA GCAGCGGACC GGGCCGGGCT GACCCCATGT	180
GGGCCGAGAG CCCGGTCCTG AGGCGGAGCT GCCGTGCGCG TCCCCCGCGG TCCCGCCCCA	240
GCGCCGGGCT CGGTCAGCAT GGATTCCTGG TTCATTCTTG TCCTGTTTGG CAGTGGTCTA	300
ATACATGTTA GTGCCAACAA TGCTACTACA GTTTCACCTT CTTTAGGAAC GACAAGATTA	360
ATTAAACAT CAACAACAGA ATTGGCTAAG GAAGAGAATA AAACCTCAAA TTCAACCTCT	420
TCAGTAATTT CTCTTTCTGT GGCACCAACA TTCAGCCCAA ACCTGACTCT GGAGCCCACC	480
TATGTGACTA CTGTTAATTC TTCACACTCT GACAATGGGA CCAGGAGGGC AGCCAGCAGC	540
GAATCTGGAG GCACTACCAT TTCCCCGAAC GGAAGCTGGC TTATTGAGAA CCAGTTCACG	600
GATGCCATAA CAGAACCCTG GGAGGGGAAC TCCAGCACTG CAGCAACCAC TCCAGAAACC	660
TTCCCCCGG CAGATGAGAC ACCAATTATT GCGGTGATGG TGGCCCTGTC CTCTCTGCTA	720
GTAATCGTGT TTATTATCAT AGTTCTGTAC ATGTTAAGGT TTAAGAAATA CAAGCAAGCT	780
GGGAGTCATT CCAACTCTTT CCGCCTGTCA AATGGCCGCA CGGAGGATGT GGAGCCCCAA	840
AGTGTAACAC TTCTGGCCAG GTCCCCGAGC ACCAACAGGA AGTACCCACC ACTGCCTGTG	900
GACAAGCTGG AAGAGGAGAT TAACCGGAGA ATGGCTGATG ACAATAAGCT CTTCAGAGAA	960
GAATTCAACG CTCTCCCTGC TTGTCTATC CAGGCCACCT GTGAGGCTGC CTCCAAGGAA	1020
GAAACAAGG AAAAAACCG CTATGTAAAC ATCCTGCCCT ATGACCACTC TAGAGTGCAC	1080
CTGACACCTG TTGAAGGGGT CCCAGATTCT GATTACATCA ACGCTTCATT CATTAAATGGC	1140
TACCAGGAAA AGAACAATT CATCGCTGCA CAAGGACCAA AAGAAGAAAC AGTGAATGAC	1200
TTCTGGAGAA TGATATGGGA ACAAACACA GCTACTATTG TCATGGTGAC CAACCTGAAG	1260
GAGAGAAAGG AGTGTAATG TGCCCAATAC TGGCCAGACC AAGGCTGCTG GACCTATGGG	1320
AATGTCCGTG TGTCTGTCTG GGATGTGACT GTTCTGGTGG ACTACACAGT ACGGAAATTC	1380
TCGATCCAGC AGGTGGGCGA CGTGACCAAC AGGAAACCAC AGCGCCTCAT CACTCAGTTC	1440
CACTTCACCA GCTGGCCAGA CTTTGGGGTG CTTTTCACCC CAATTGGCAT GCTCAAGTTC	1500
CTCAAGAAGG TGAAGGCCTG TAACCCTCAG TACGCAGGGG CTATCGTGGT CCACTGCAGT	1560
GCAGGTGTAG GGCGCACTGG CACCTTTGTT GTCATCGATG CCATGCTGGA CATGATGCAT	1620
TCGGAGCGCA AAGTGGATGT ATATGGGTTT GTGAGCCGGA TCCGGGCCCCA GCGCTGCCAG	1680
ATGGTACAGA CAGACATGCA GTACGTCTTC ATATACCAGG CCCTTCTGGA GCATTATCTG	1740
TATGGGGACA CAGAACTGGA AGTGACTTCT CTAGAAACCC ACCTACAAA AATTATAAC	1800
AAGATCCCGG GGAAGTAGCA CAACGGGTGA GAGGAGGAGT TTAAGAAATT AACTTCAATC	1860
AAAATCCAGA ATGACAAGAT GCGCACGGGA AACCTTCCAG CCAACATGAA GAAGAACCGG	1920

GTTTTACAGA TCATTCCATA TGAATTTAAC AGAGTGATCA TTCCAGTCAA ACGAGGCGAA	1980
GAGAACACAG ACTATGTGAA CGCATCCTTC ATTGATGGAT ACCGGCAGAA AGACTCCTAC	2040
ATTGCCAGCC AGGGCCCTCT TCTCCACACG ATTGAGGACT TCTGGCGAAT GATCTGGGAG	2100
TGGAAGTCCT GTTCTATCGT AATGCTGACA GAACTGGAAG AGAGAGGCCA GGAGAAGTGT	2160
GCCCAGTACT GGCCATCTGA TGGCCTGGTG TCCTACGGAG ACATCACAGT TGAGCTGAAG	2220
AAGGAGGAGG AATGTGAAAG CTACACTGTC CGAGACCTCC TGGTCACCAA CACCAGGGAG	2280
AACAAGAGTC GGCAAATCCG GCAGTTCCAC TTCCACGGCT GGCCTGAGGT GGGCATCCCC	2340
AGCGACGGCA AGGGCATGAT CAACATCATT GCAGCAGTGC AGAAGCAGCA GCAGCAGTCG	2400
GGGAACCATC CCATCACTGT GCACTGCAGT GCCGGGGCAG GACGGACAGG AACCTTCTGT	2460
GCCTTGAGCA CAGTCCTGGA ACGTGTGAAA GCAGAAGGAA TTTTAGATGT CTTCCAAACT	2520
GTCAAGAGCC TCGGGCTGCA GAGGCCACAC ATGGTCCAGA CACTGGAACA GTATGAATTC	2580
TGCTACAAGG TGGTACAGGA ATACATTGAC GCCTTTTCAG ATTATGCCAA CTTCAAGTGA	2640
CAGGTGACAA GGCCCACAGA CAGGAGAATT GCCTTTAATA TTTTGTAATA TTCTGTTTTT	2700
GTTAATATAC CCAAATTGT ATATATCTTA TAACTGTTTT AGAAATGGCA CATAGGCTTC	2760
TATTACCTGT TAGATGGAGA TTTTGTATGT AAATGTGTTA GCACTGATAG TCCTTTTCCA	2820
GTGTTTTATT GGGAAATTAA TAGTGTGATA TTTGGGTTGA TATAATGAAT TC	2872

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn	Gln	Asn	Lys	Asn	Arg	Tyr	Val	Asp	Ile	Leu	Pro	Tyr	Asp	Tyr	Asn
1				5					10					15	
Arg	Val	Glu	Leu	Ser	Glu	Ile	Asn	Gly	Asp	Ala	Gly	Ser	Asn	Tyr	Ile
		20						25					30		
Asn	Ala	Ser	Tyr	Ile	Asp	Gly	Phe	Lys	Glu	Pro	Arg	Lys	Tyr	Ile	Ala
		35					40					45			
Ala	Gln	Gly	Pro	Arg	Asp	Glu	Thr	Val	Asp	Asp	Phe	Trp	Arg	Met	Ile
	50				55					60					
Trp	Glu	Gln	Lys	Ala	Thr	Val	Ile	Val	Met	Val	Thr	Arg	Cys	Glu	Glu
65				70					75					80	
Gly	Asn	Arg	Asn	Lys	Cys	Ala	Glu	Tyr	Trp	Pro	Ser	Met	Glu	Glu	Gly
			85						90					95	
Thr	Arg	Ala	Phe	Gly	Asp	Val	Val	Val	Lys	Ile	Asn	Gln	His	Lys	Arg
		100						105					110		
Cys	Pro	Asp	Tyr	Ile	Ile	Gln	Lys	Leu	Asn	Ile	Val	Asn	Lys	Lys	Glu

115	120	125
Lys Ala Thr Gly Arg Glu Val Thr His Ile Gln Phe Thr Ser Trp Pro		
130	135	140
Asp His Gly Val Pro Glu Asp Pro His Leu Leu Leu Lys Leu Arg Arg		
145	150	155
Arg Val Asn Ala Phe Ser Asn Phe Phe Ser Gly Pro Ile Val Val His		
165	170	175
Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Tyr Ile Gly Ile Asp Ala		
180	185	190
Met Leu Glu Gly Leu Glu Ala Glu Asn Lys Val Asp Val Tyr Gly Tyr		
195	200	205
Val Val Lys Leu Arg Arg Gln Arg Cys Leu Met Val Gln Val Glu Ala		
210	215	220
Gln Tyr Ile Leu Ile His Gln Ala Leu Val Glu		
225	230	235

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 236 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser	
1	5
Arg Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile	
20	25
Asn Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala	
35	40
Ala Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile	
50	55
Trp Glu Gln Asn Thr Ala Thr Ile Val Met Val Thr Asn Leu Lys Glu	
65	70
Arg Lys Glu Cys Lys Cys Ala Gln Tyr Trp Pro Asp Gln Gly Glu Trp	
85	90
Thr Tyr Gly Asn Ile Arg Val Ser Val Glu Asp Val Thr Val Leu Val	
100	105
Asp Tyr Thr Val Arg Lys Phe Cys Ile Gln Gln Val Gly Asp Met Thr	
115	120
Asn Arg Lys Pro Gln Arg Leu Ile Thr Gln Phe His Phe Thr Ser Trp	
130	135
Pro Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu	
145	150
Lys Lys Val Lys Ala Cys Asn Pro Gln Tyr Ala Gly Ala Ile Val Val	

	165		170		175
His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Val Val Ile Asp					
	180		185		190
Ala Met Leu Asp Met Met His Thr Glu Arg Lys Val Asp Val Tyr Gly					
	195		200		205
Phe Val Ser Arg Ile Arg Ala Gln Arg Cys Gln Met Val Gln Thr Asp					
	210		215		220
Met Gln Tyr Val Phe Ile Tyr Gln Ala Leu Leu Glu					
	225		230		235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Val Ala Tyr Asp His Ser	
1 5 10 15	
Arg Val Lys Leu Ala Gln Leu Ala Glu Lys Asp Gly Lys Leu Thr Asp	
20 25 30	
Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Arg Pro Lys Ala Tyr	
35 40 45	
Ile Ala Ala Gln Gly Pro Leu Lys Ser Thr Ala Glu Asp Phe Trp Arg	
50 55 60	
Met Ile Trp Glu His Asn Val Glu Val Ile Val Met Ile Thr Asn Leu	
65 70 75 80	
Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Ala Asp Gly	
85 90 95	
Ser Glu Glu Tyr Gly Asn Phe Leu Val Thr Gln Lys Ser Val Gln Val	
100 105 110	
Leu Ala Tyr Tyr Thr Val Arg Asn Phe Thr Leu Arg Asn Thr Lys Ile	
115 120 125	
Lys Lys Gly Ser Gln Lys Gly Arg Pro Ser Gly Arg Val Val Thr Gln	
130 135 140	
Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu Tyr Ser Leu	
145 150 155 160	
Pro Val Leu Thr Phe Val Arg Lys Ala Ala Tyr Ala Lys Arg His Ala	
165 170 175	
Val Gly Pro Val Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly	
180 185 190	
Thr Tyr Ile Val Leu Asp Ser Met Leu Gln Gln Ile Gln His Glu Gly	
195 200 205	
Thr Val Asn Ile Phe Gly Phe Leu Lys His Ile Arg Ser Gln Arg Asn	

210	215	220
Tyr Leu Val Gln Thr Glu Gln Tyr Val Phe Ile His Asp Thr Leu		
225	230	235 240
Val Glu		

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 245 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Lys His Lys Asn Arg Tyr Ile Asn Ile Leu Ala Tyr Asp His Ser	
1 5 10 15	
Arg Val Lys Leu Arg Pro Leu Pro Gly Lys Asp Ser Lys His Ser Asp	
20 25 30	
Tyr Ile Asn Ala Asn Tyr Val Asp Gly Tyr Asn Lys Ala Lys Ala Tyr	
35 40 45	
Ile Ala Thr Gln Gly Pro Leu Lys Ser Thr Phe Glu Asp Phe Trp Arg	
50 55 60	
Met Ile Trp Glu Gln Asn Thr Gly Ile Ile Val Met Ile Thr Asn Leu	
65 70 75 80	
Val Glu Lys Gly Arg Arg Lys Cys Asp Gln Tyr Trp Pro Thr Glu Asn	
85 90 95	
Ser Glu Glu Tyr Gly Asn Ile Ile Val Thr Leu Lys Ser Thr Lys Ile	
100 105 110	
His Ala Cys Tyr Thr Val Arg Arg Phe Ser Ile Arg Asn Thr Lys Val	
115 120 125	
Lys Lys Gly Gln Lys Gly Asn Pro Lys Gly Arg Gln Asn Glu Arg Val	
130 135 140	
Val Ile Gln Tyr His Tyr Thr Gln Trp Pro Asp Met Gly Val Pro Glu	
145 150 155 160	
Tyr Ala Leu Pro Val Leu Thr Phe Val Arg Arg Ser Ser Ala Ala Arg	
165 170 175	
Met Pro Glu Thr Gly Pro Val Leu Val His Cys Ser Ala Gly Val Gly	
180 185 190	
Arg Thr Gly Thr Tyr Ile Val Ile Asp Ser Met Leu Gln Gln Ile Lys	
195 200 205	
Asp Lys Ser Thr Val Asn Val Leu Gly Phe Leu Lys His Ile Arg Thr	
210 215 220	
Gln Arg Asn Tyr Leu Val Gln Thr Glu Glu Gln Tyr Ile Phe Ile His	
225 230 235 240	
Asp Ala Leu Leu Glu	
245	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: /label= Xaa  
/note= "For the Consensus Sequence, Xaa = Lack of Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

Asn Lys His Lys Asn Arg Tyr Xaa Asn Ile Leu Xaa Tyr Asp His Ser
1      5      10      15
Arg Val Lys Leu Xaa Xaa Leu Xaa Xaa Lys Xaa Xaa Lys Xaa Ser Asp
20      25      30
Tyr Ile Asn Ala Xaa Tyr Xaa Asp Gly Tyr Asn Glu Pro Lys Xaa Tyr
35      40      45
Ile Ala Ala Gln Gly Pro Leu Lys Xaa Thr Val Glu Asp Phe Trp Arg
50      55      60
Met Ile Trp Glu Gln Asn Thr Xaa Val Ile Val Met Xaa Thr Asn Leu
65      70      75      80
Val Glu Lys Gly Arg Arg Lys Cys Xaa Gln Tyr Trp Pro Xaa Xaa Gly
85      90      95
Ser Glu Xaa Tyr Gly Asn Ile Xaa Val Thr Val Lys Xaa Val Xaa Val
100     105     110
Leu Ala Xaa Xaa Asp Tyr Thr Val Arg Lys Phe Xaa Xaa Arg Asn Thr
115     120     125
Lys Ile Xaa Lys Xaa Gly Xaa Lys Xaa Xaa Xaa Lys Gly Arg Xaa Xaa
130     135     140
Gly Arg Val Val Thr Gln Tyr His Xaa Thr Xaa Trp Pro Asp Met Gly
145     150     155     160
Val Pro Glu Tyr Pro Leu Pro Val Leu Xaa Phe Val Arg Xaa Val Xaa
165     170     175
Ala Ala Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Val Val His Cys Ser Ala
180     185     190
Gly Val Gly Arg Thr Gly Thr Tyr Ile Val Ile Asp Xaa Met Leu Gln
195     200     205
Gln Ile Xaa Xaa Glu Xaa Xaa Val Xaa Val Tyr Gly Phe Xaa Lys His
210     215     220
Ile Arg Xaa Gln Arg Xaa Tyr Xaa Val Gln Thr Glu Glu Gln Tyr Xaa
225     230     235     240
Phe Ile His Xaa Ala Leu Xaa Glu
245

```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asn	Lys	Ser	Lys	Asn	Arg	Asn	Ser	Asn	Val	Ile	Pro	Tyr	Asp	Tyr	Asn	1	5	10	15
Arg	Val	Pro	Leu	Lys	His	Glu	Leu	Glu	Met	Ser	Lys	Glu	Ser	Glu	His	20	25	30	
Asp	Ser	Asp	Glu	Ser	Ser	Asp	Asp	Asp	Ser	Asp	Ser	Glu	Glu	Pro	Ser	35	40	45	
Lys	Tyr	Ile	Asn	Ala	Ser	Phe	Ile	Met	Ser	Tyr	Trp	Lys	Pro	Glu	Val	50	55	60	
Met	Ile	Ala	Ala	Gln	Gly	Pro	Leu	Lys	Glu	Thr	Ile	Gly	Asp	Phe	Trp	65	70	75	80
Gln	Met	Ile	Phe	Gln	Arg	Lys	Val	Lys	Val	Ile	Val	Met	Leu	Thr	Glu	85	90	95	
Leu	Lys	His	Gly	Asp	Gln	Glu	Ile	Cys	Ala	Gln	Tyr	Trp	Gly	Glu	Gly	100	105	110	
Lys	Gln	Thr	Tyr	Gly	Asp	Ile	Glu	Val	Asp	Leu	Lys	Asp	Thr	Asp	Lys	115	120	125	
Ser	Ser	Thr	Tyr	Thr	Leu	Arg	Val	Phe	Glu	Leu	Arg	His	Ser	Lys	Arg	130	135	140	
Lys	Asp	Ser	Arg	Thr	Val	Tyr	Gln	Tyr	Gln	Tyr	Thr	Asn	Trp	Ser	Val	145	150	155	160
Glu	Gln	Leu	Pro	Ala	Glu	Pro	Lys	Glu	Leu	Ile	Ser	Met	Ile	Gln	Val	165	170	175	
Val	Lys	Gln	Lys	Leu	Pro	Gln	Lys	Asn	Ser	Ser	Glu	Gly	Asn	Lys	His	180	185	190	
His	Lys	Ser	Thr	Pro	Leu	Leu	Ile	His	Cys	Arg	Asp	Gly	Ser	Gln	Gln	195	200	205	
Thr	Gly	Ile	Phe	Cys	Ala	Leu	Leu	Asn	Leu	Leu	Glu	Ser	Ala	Glu	Thr	210	215	220	
Glu	Glu	Val	Val	Asp	Ile	Phe	Gln	Val	Val	Lys	Ala	Leu	Arg	Lys	Ala	225	230	235	240
Arg	Pro	Gly	Met	Val	Ser	Thr	Phe	Glu	Gln	Tyr	Gln	Phe	Leu	Tyr	Asp	245	250	255	
Val	Ile	Ala	Ser													260			

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 233 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Asn Met Lys Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn
1      5      10      15
Arg Val Ile Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val
20      25      30
Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala
35      40      45
Ser Gln Gly Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile
50      55      60
Trp Glu Trp Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Glu
65      70      75      80
Arg Gly Gln Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val
85      90      95
Ser Tyr Gly Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu
100     105     110
Ser Tyr Thr Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys
115     120     125
Ser Arg Gln Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly
130     135     140
Ile Pro Ser Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln
145     150     155     160
Lys Gln Gln Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser
165     170     175
Ala Gly Ala Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu
180     185     190
Glu Arg Val Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys
195     200     205
Ser Leu Ala Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr
210     215     220
Glu Phe Cys Tyr Lys Val Val Gln Glu
225     230

```

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 234 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:



```

Asn Arg Glu Lys Asn Arg Thr Ser Ser Ile Ile Pro Val Glu Arg Ser
1      5      10      15
Arg Val Gly Ile Ser Ser Leu Ser Gly Glu Gly Thr Asp Tyr Ile Asn
      20      25      30
Ala Ser Tyr Ile Met Gly Tyr Tyr Gln Ser Asn Glu Phe Ile Ile Thr
      35      40      45
Gln His Pro Leu Leu His Thr Ile Lys Asp Phe Trp Arg Met Ile Trp
      50      55      60
Asp His Asn Ala Gln Leu Val Val Met Ile Pro Asp Gly Gln Asn Met
      65      70      75      80
Ala Glu Asp Glu Phe Val Tyr Trp Pro Asn Lys Asp Glu Pro Ile Asn
      85      90      95
Cys Glu Ser Phe Lys Val Thr Leu Met Ala Glu Glu His Lys Cys Leu
      100      105      110
Ser Asn Glu Glu Lys Leu Ile Ile Gln Asp Phe Ile Leu Glu Ala Thr
      115      120      125
Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys Trp
      130      135      140
Pro Asn Pro Asp Ser Pro Ile Ser Lys Thr Phe Glu Leu Ile Ser Val
      145      150      155      160
Ile Lys Glu Glu Ala Ala Asn Arg Asp Gly Pro Met Ile Val His Asp
      165      170      175
Glu His Gly Gly Val Thr Ala Gly Thr Phe Cys Ala Leu Thr Thr Leu
      180      185      190
Met His Gln Leu Glu Lys Glu Asn Ser Val Asp Val Tyr Gln Val Ala
      195      200      205
Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Ala Asp Ile Glu Gln
      210      215      220
Tyr Gln Phe Leu Tyr Lys Val Ile Leu Ser
      225      230

```

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 235 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Asn Lys Glu Lys Asn Arg Asn Ser Ser Val Val Pro Ser Glu Arg Ala
1      5      10      15
Arg Val Gly Leu Ala Pro Leu Pro Gly Met Lys Gly Thr Asp Tyr Ile
      20      25      30
Asn Ala Ser Tyr Ile Met Gly Tyr Tyr Arg Ser Asn Glu Phe Ile Ile
      35      40      45

```

Thr Gln His Pro Leu Pro His Thr Thr Lys Asp Phe Trp Arg Met Ile  
50 55 60

Trp Asp His Asn Ala Gln Ile Ile Val Met Leu Pro Asp Asn Gln Ser  
65 70 75 80

Leu Ala Glu Asp Glu Phe Val Tyr Trp Pro Ser Arg Glu Glu Ser Met  
85 90 95

Asn Cys Glu Ala Phe Thr Val Thr Leu Ile Ser Lys Asp Arg Leu Cys  
100 105 110

Leu Ser Asn Glu Glu Gln Ile Ile Ile His Asp Phe Ile Leu Glu Ala  
115 120 125

Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys  
130 135 140

Trp Pro Asn Pro Asp Ala Pro Ile Ser Ser Thr Phe Glu Leu Ile Asn  
145 150 155 160

Val Ile Lys Glu Glu Ala Leu Thr Arg Asp Gly Pro Thr Ile Val His  
165 170 175

Asp Glu Tyr Gly Ala Val Ser Ala Gly Met Leu Cys Ala Leu Thr Thr  
180 185 190

Leu Ser Gln Gln Leu Glu Asn Glu Asn Ala Val Asp Val Phe Gln Val  
195 200 205

Ala Lys Met Ile Asn Leu Met Arg Pro Gly Val Phe Thr Asp Ile Glu  
210 215 220

Gln Tyr Gln Phe Ile Tyr Lys Ala Arg Leu Ser  
225 230 235

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Modified-sites
- (B) LOCATION: 1..280
- (D) OTHER INFORMATION: /label= Xaa  
/note= "For the Consensus Sequence, Xaa = Lack of  
Consensus"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Lys Glu Lys Asn Arg Asn Ser Ser Xaa Ile Pro Tyr Glu Arg Asn  
1 5 10 15

Arg Val Gly Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Glu Glu Gly Thr  
35 40 45

Asp Tyr Ile Asn Ala Ser Xaa Ile Met Gly Tyr Tyr Gln Ser Asn Glu  
50 55 60

Phe Ile Xaa Thr Gln Xaa Pro Leu Leu His Thr Ile Lys Asp Phe Trp  
 65 70 75 80  
 Arg Met Ile Trp Asp His Xaa Asn Ala Gln Ile Val Met Leu Xaa Xaa  
 85 90 95  
 Xaa Gln Xaa Xaa Ala Glu Xaa Glu Xaa Xaa Gln Tyr Trp Pro Ser Xaa  
 100 105 110  
 Gly Xaa Xaa Xaa Tyr Gly Asp Xaa Xaa Val Xaa Leu Lys Xaa Xaa Xaa  
 115 120 125  
 Asn Cys Glu Ser Xaa Thr Val Thr Xaa Xaa Xaa Glu Xaa Arg Xaa Cys  
 130 135 140  
 Leu Ser Asn Glu Xaa Arg Xaa Ile Ile Gln Asp Phe Ile Leu Glu Ala  
 145 150 155 160  
 Thr Gln Asp Asp Tyr Val Leu Glu Val Arg His Phe Gln Cys Pro Lys  
 165 170 175  
 Trp Pro Asn Pro Asp Xaa Pro Ile Ser Xaa Thr Xaa Glu Leu Ile Ser  
 180 185 190  
 Val Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Lys Xaa Glu Glu Ala  
 195 200 205  
 Xaa Asn Arg Xaa Xaa Xaa Asp Gly Pro Xaa Ile Val His Xaa Glu Xaa  
 210 215 220  
 Gly Ala Val Xaa Xaa Gly Thr Phe Cys Ala Leu Thr Thr Leu Leu Glu  
 225 230 235 240  
 Gln Leu Glu Xaa Glu Asn Xaa Val Asp Val Phe Gln Val Xaa Lys Met  
 245 250 255  
 Xaa Asn Leu Met Arg Pro Gly Xaa Xaa Xaa Xaa Ile Glu Gln Tyr Gln  
 260 265 270  
 Phe Leu Tyr Lys Val Ile Leu Ser  
 275 280